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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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February 11, 2003, 19:46:30 ; Search time 142.457 Seconds (without alignments) 2118.076 Million cell updates/sec OM protein - protein search, using sw model Run on:

US-09-497-967-7 2540 1 MKNNILVILIISLEINQIKS......QCDFANFLSISLLISYXLL 468 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

4569144 seqs, 644733110 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Pending\_Patents\_AA\_Main:\*

1: /cgn2\_6/ptodata/1/paa/PCTUS\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/paa/USO6\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/paa/USO6\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/paa/USO8\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/paa/USO81\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/paa/USO81\_COMB.pep:\*

7: /cgn2\_6/ptodata/1/paa/USO82\_COMB.pep:\*

9: /cgn2\_6/ptodata/1/paa/USO84\_COMB.pep:\*

10: /cgn2\_6/ptodata/1/paa/USO84\_COMB.pep:\*

11: /cgn2\_6/ptodata/1/paa/USO84\_COMB.pep:\*

12: /cgn2\_6/ptodata/1/paa/USO84\_COMB.pep:\*

13: /cgn2\_6/ptodata/1/paa/USO84\_COMB.pep:\*

13: /cgn2\_6/ptodata/1/paa/USO84\_COMB.pep:\*

14: /cgn2\_6/ptodata/1/paa/USO82\_COMB.pep:\*

15: /cgn2\_6/ptodata/1/paa/USO82\_COMB.pep:\*

16: /cgn2\_6/ptodata/1/paa/USO92\_COMB.pep:\*

17: /cgn2\_6/ptodata/1/paa/USO92\_COMB.pep:\*

18: /cgn2\_6/ptodata/1/paa/USO92\_COMB.pep:\*

19: /cgn2\_6/ptodata/1/paa/USO93\_COMB.pep:\*

10: /cgn2\_6/ptodata/1/paa/USO93\_COMB.pep:\* /cgn2\_6/ptodata/1/paa/US097\_COMB.pep:\*
/cgn2\_6/ptodata/1/paa/US098\_COMB.pep:\*
/cgn2\_6/ptodata/1/paa/US090\_COMB.pep:\*
/cgn2\_6/ptodata/1/paa/US100\_COMB.pep:\*
/cgn2\_6/ptodata/1/paa/US102\_COMB.pep:\*
/cgn2\_6/ptodata/1/paa/US102\_COMB.pep:\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/cgn2\_6/ptodata/1/paa/US60\_COMB.pep:\*

Description	Sequence 7, Appli Sequence 6, Appli Sequence 54, Appl Sequence 6, Appli Sequence 5, Appli Sequence 15, Appli
SUMMARIES nigth DB ID	US-09-497-967-7 US-09-498-612-6 US-09-497-967-54 US-09-497-967-6 US-09-498-612-5 US-07-763-352A-15
DB	18 18 18 3
Length	4 4 4 6 8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
Query Ove Match Length DB II	100.0 100.0 99.7 36.3 36.3
Score	2540 2540 2533 921 921 843.5
Result No.	H CA W & W P

equence 61, quence 3, A equence 57, equence 58, equence 60, equence 60,	equence 59, equence 301 equence 301 equence 301 equence 301, equence 301, equence 301, equence 301,		equence 343, equence 343, equence 343, equence 343, equence 343, equence 69, e
09-497-967 09-497-967 09-497-967 09-497-967 09-497-967 09-497-967	22-497-967 (0-123-155 (0-140-472 0-140-865 (0-141-756 0-141-759	0-142-426 0-142-885- 0-142-885- 0-158-791 0-137-871 0-140-805- 0-140-905- 0-141-756-	0-141-759 0-141-761 0-142-8456 0-142-8456 0-146-731 0-158-790 0-179-524 0-184-634
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## ALIGNMENTS

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Sequence 7, Application US/09497967

Sequence 7, Application US/09497967

GENERAL INFORMATION:

APPLICANT: Dickerson, Jr., Harry W.

APPLICANT: Dickerson, Jr., Harry W.

APPLICANT: Lin, Tian-Long

TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF

TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF

TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF

TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF

TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF

FILENCE REPRESSION NUMBER: 60/131,121

PRIOR PLILING DATE: 1999-02-04

PRIOR FILING DATE: 1999-02-04

PRIOR FILING DATE: 1999-03-07

PRIOR APPLICATION NUMBER: 60/124,905

PRIOR APPLICATION NUMBER: 60/124,905

PRIOR APPLICATION NUMBER: 60/124,905

PRIOR PLILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 102

SOFTWARE: PATENTIN VEY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Ichthyophthirius multifillis US-09-497-967-7
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LENGTH: 468
TYPE: PRT
US-09-497-967-7
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100.0%; Score 2540; DB 18; Length 468;

Query Match

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MKNNILVILIISLFINQIKSANCPVGTETNTAGQYDDLGTPANCVNCQKNFYYNNAAAFV
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Best Local Similarity 99.8%;
Matches 467; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 102
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LENGTH: 468
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APPLICANT: CLARK, Theodore G.
APPLICANT: CLARK, Theodore G.
APPLICANT: THE UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC
TITLE OF INVENTION: RECOMBINANT EXPRESSION OF HETEROLOGOUS NUCLEIC ACIDS IN
TITLE OF INVENTION: PROTOZOA
TITLE OF INVENTION: PROTOZOA
TITLE OF INVENTION: PROTOZOA
TITLE OF INVENTION: PROTOZOA
TITLE OF INVENTION: DATE: 2000-02-04
CURRENT APPLICATION NUMBER: 06/118,634
PRIOR APPLICATION NUMBER: 60/112,372
PRIOR APPLICATION NUMBER: 60/122,372
PRIOR FILING DATE: 1999-03-17
PRIOR FILING DATE: 1999-03-17
PRIOR FILING DATE: 1999-03-17
PRIOR FILING DATE: 1999-03-17
PRIOR APPLICATION NUMBER: 60/131,121
PRIOR PILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: CO/131,121
PRIOR PILING DATE: 1999-04-27
PRIOR PILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: CO/131,020
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                         Indels
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100.0%; Pred. No. 6.9e-213;
tive 0; Mismatches 0;
           Pred. No. 6.9e-213;
; Mismatches 0;
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       100.08; F1
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               Similarity 100.
8; Conservative
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SOFTWARE: Patentin Ver.
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US-09-498-612-6
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Best Local 3
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               Best Local
Matches 46
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APPLICANT: Clark, Theodore G.
APPLICANT: Clark, Theodore G.
APPLICANT: Clark, Tan-Long
APPLICANT: Lin, Tian-Long
TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF
TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF
TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF
TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF
TITLE OF INVENTION: DIAGNOSTIC AND PROTECTION UNBER: US/09/497,967
CURRENT FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 60/131,121
PRIOR PILING DATE: 1999-02-04.27
PRIOR FILING DATE: 1999-03-04.27
PRIOR APPLICATION NUMBER: 60/122,372
PRIOR PLING DATE: 1999-03-03-07
PRIOR APPLICATION NUMBER: 60/124,905
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Pred. No. 2.8e-212;
0; Mismatches 1;
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GENERAL INFORMATION:
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US-09-49/-967-6
Sequence 6, Application US/09497967
GENERAL INFORMATION:
APPLICANT: Clark, Theodore G.
APPLICANT: Dickerson, Jr., Harry W.
APPLICANT: Lin, Tian-Long
TITLE OF INVENTION: ICHTWOPHTHIRUGS
TITLE OF INVENTION: ICHTWOPHTHIRUGS
FILE REFERENCE: 235.001701101
CURRENT APPLICATION NUMBER: US/09/497,967
FILE REFERENCE: 235.001701101
CURRENT FILING DATE: 1999-04-27
FRIOR APPLICATION NUMBER: 60/131,121
PRIOR FILING DATE: 1999-02-04
PRIOR FILING DATE: 1999-02-04
PRIOR FILING DATE: 1999-03-07
PRIOR FILING DATE: 1999-03-17
SOFTWARE: PALCATION NUMBER: 60/122,372
PRIOR FILING DATE: 1999-03-17
SOFTWARE: PALCATION NUMBER: 60/124,905
NUMBER OF SEQ ID NOS: 102
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                 AATLAKQCNIACPDGTAIASGATNYVILQTECLNCAANFYFDGNNFQAGSSRCKACPANK 360
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                                                       RSFTECVKCRLNFYYNGNNGNTPFNPGKSQCTPCPAIKPANVAQATLGNDATITAQCNVA
                                                                                                               241 CPDGTISAAGVNNWVAQNTECINCAPNFYNNNAPNFNPGNSTCLPCPANKDYGAEATAGG
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36.3%; Score 921; DB 18; Length 442;
Best Local Similarity 41.8%; Pred. No. 2.2e-71;
Matches 214; Conservative 45; Mismatches 139; Indels 11:
                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Ichthyophthirius multifiliis
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APPLICANT: GARRIG, Jacek
APPLICANT: DICKERSON Jr., Harry W.
APPLICANT: CLARK, Theodore G.
APPLICANT: CLARK, Theodore G.
APPLICANT: CLARK, THEOGORE B.
TITLE OF INVENTION: PROTOZOA
TITLE OF INVENTION: PROTOZOA
TITLE OF INVENTION: PROTOZOA
FILE REPERENCE: 235.00100101
CURRENT FILING DATE: 2000-02-04
CURRENT FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: 60/118,634
PRIOR PRIOR PELING DATE: 1999-03-07
PRIOR PELING DATE: 1999-03-07
PRIOR PELING DATE: 1999-03-07
PRIOR PELING DATE: 1999-04-07
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 14
SEQ ID NO 5
FRONTHARE PARENTIN VEY: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19;
                                                                    APN---FNPG-----NSTCLPCPANKDYGAEATAGGAATLAKQCNIACPDGTAIAS 320
                                                                                       293 GVILVESNSSTQCSQCIANYFFNG-NFEAGKSQCLKCPVSKTTPAHA-PGNTATQATQCL 350
                                                                                                                                                                                                            380 LECPAGIVLIDGIISTYKQAASECVKCAANFYTIKQIDWVAGIDICISCNKKLISGAEAN 439
                                                                                                                                                                                                                                57 AAFVPGASTCTPCPQKKDAGAQPNPPATANLVTQCNVKCPAGTAIAGGATDYAAIITECV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 NCRINFYNENAPNFNAGASTCTACPVNRVGGALTAGNAATIVAQCNVACPTGTALDDGVT 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .77 TDYVRSFTECVKCRLNFYYNGNN--GNTP----FNPG-----KSOCTPCPAIKPAN 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MKNNILVILIISLFINQIKSANCPVGTETNTAGQVD----DLGTPANCVNCQKNFYYNNA 56
                                                                                                                                       GAT-NYVILQTECLNCAANFYFDGNNFQAGSSRCKACPANKVQGAVATAGGTATLIAQCA
                      57 AA------QGEANGNOPFAAN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 114;
222 VAQATLGNDATITAQCNVACPDGTISAAGVNNWVAQNTE---CTNCAPNFYNN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 36.3%; Score 921; DB 18; Best Local Similarity 41.8%; Pred. No. 2.2e-71; Matches 214; Conservative 45; Mismatches 139;
                                                                                                                                                                                                                                                                              LPESAKKNIQC---DFANFLSISLLLISYYLL 468
                                                                                                                                                                                                                                                                                                   ORGANISM: Ichthyophthirius multifillis
                                                                                                                                                                                                                                                                                                                                                                                    US-09-498-612-5; Sequence 5, Application US/09498612; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-498-612-5
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                                                                                                              321 GAT-NYVILQTECLNCAANFYFDGNNFQAGSSRCKACPANKVQGAVATAGGTATLIAQCA 379
                                                                                                                              222 VAQATLGNDATITAQCNVACPDGTISAAGVNNWVAQNTE---CTNCAPNEYNN----N 272
                         176 DSPATAGAQANLATQCSNQCPTGTVLDDGVT--LVFNTSATLCVKCRPNFYYNGGSPQGE 233
                                                       APN---FNPG-----NSTCLPCPANKDYGAEATAGGAATLAKQCNIACPDGTAIAS 320
                                                                         380 LECPAGTVLTDGTTSTYKQAASECVKCAANFYTTKQTDWVAGIDTCTSCNKKLTSGAEAN 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKNNILVILIISLFINQIKSANCPVGTETNTAGQVD----DLGTPANCVNCQKNFYYNNA 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 414;
                                                                                                                                                                                                                                                                                                                      Sequence 15, Application US/07763352A
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GICKERSON:
TILLE OF INVENTION:
TILLE OF INVENTION:
TILLE OF INVENTION:
UNMARR OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.2%; Score 843.5;
40.9%; Pred. No. 1.2e
Live 41; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         Greenlee and Winner
5370 Manhattan Circle, Ste. 201
                                                                                                                                                                                                                               440 LPESAKKNIQC---DFANFLSISLLLISYYLL 468
                                                                                                                                                                                                                                             SOUTHWARE: TEACHLIANT APPLICATION DATA:
APPLICATION NUMBER: US/07/763,352A
FILING DATE: 19910920
CLASSIFFCATION: 435
ATTORNEY,AGENT INFORMATION:
NAME: FEACH. DOING M.
RECISTRATION NUMBER: 33,878
RECISTRATION NUMBER: 33,878
TELECOMMUNICATION INFORMATION:
TELEPAX: 303/499-8089
TELEFAX: 303/499-8089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 303/499-8089
TELEX: 823189
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 414 amino acids TYPE: AMINO ACID
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 5370 MC CITY: Boulder STATE: Colorado
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-763-352A-15
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Best Local Simi
Matches 196;
                                                                                                                                                                                                                                                                                                        RESULT 6
US-07-763-352A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 ACPVNRVGGALTAGNAATIVAQCNVACPTGTALDDGVTTDYVRSFTECVKCRLNFYYNGN 198
                                                                                                                                                                                                               273 APN---FNPG-----NSTCLPCPANKDYGAEATAGGAATLAKQCNIACPDGTAIAS 320
                                                                                                                                                                                                                                   GAT-NYVILQTECLNCAANFYFDGNNFQAGSSRCKACPANKVQGAVATAGGTATLIAQCA 379
                                                                                                                                                                                                                                                                                                        222 VAQATLGNDATITAQCNVACPDGTISAAGVNNWVAQNTE---CINCAPNFYNN-----N 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 CPVGTETNTAGQVD----DLGTPANCVNCQKNFYYNNAAAFVPGASTCTPCPQKKDAGAQ 78
NCRINFYNENAPNFNAGASTCTACPVNRVGGALTAGNAATIVAQCNVACPTGTALDDGVT 176
                                                                                                                                                             -----naargicvpcqinrygsvtnagdlatlatqcstqcptgtalddgvt 117
                                                                     TDYVRSFTECVKCRLNFYYNGNN--GNTP----FNPG-----KSQCTPCPAIKPAN 221
                                                                                                                                                                                                                                                                                                                                                      380 LECPAGTVLIDGTISTYKQAASECVKCAANFYTTKQIDWVAGIDTCTSCNKKLISGAEA 438
                                                                                                                                                                                                                                                                                                                                                                       -----NAARGICV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 CPDGTQTQ-AGLTDVGAADLGT---CVNCRPNFYYNGGAA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/124,905
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 61, Application US/09497967 GENERAL INFORMATION:
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ARGICVPCQINRVGSVTNAGDLATLATQCSTQCPTGTALDDGVTDVFDRSAAQCVKCKPN 117
                                                                                                                                                                                                                                                       411 YTTKQTDWVAGIDTCTSCNKKLTSGAEA 438
                                                                                                                                                                                                                                                                           ORGANISM: Ichthyophthirius multifiliis
                                                                                                                                                                                                                                                                                                                                                             Sequence 57, Application US/09497967 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
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LENGTH: 76
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Best Local Si
Matches 76;
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       ---NAPN---FNPG-----NST 282
                   341
                                                                         342 DGNNFQAGSSRCKACPANKVQGAVATAGGTATLIAQCALECPAGTVLTDGTTSTYKQAAS 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 KDAGAQPNPPATANLVTQCNVKCPAGTAIAGGATDYAAIITECVNCRINFYNENAPNFNA 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 GASTCTACPVNRVGGALTAGNAATIVAQCNVACPTGTALDDGVTTDYVRSFTECVKCRLN 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29.5%; Score 749; DB 3; Length 375;
38.4%; Pred. No. 1.9e-56;
1ve 39; Mismatches 133; Indels 104; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 QIKSANCPVGTETNTAGQVD----DLGTPANCVNCQKNFYYNNAAAFVPGASTCTPCPQK 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----NA 57
                                                        CLPCPANKDYGAEATAGGAATLAKQCNIACPDGTAIASGAT-NYVILQTECLNCAANFYF
                                                                                                                                                                     ECVKCAANFYTTKQTDWVAGIDTCTSCNKKLTSGAEANLPESAKKNIQCDFANF 455
                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Clark, Theodore G.
APPLICANT: Clark, Theodore G.
APPLICANT: Clark, Theodore G.
TITLE OF INVENTION: ICH IMMOBILIZATION ANTIGEN AND FISH
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Greenlee and Winner
STREET: 5370 Manhattan Circle, Ste. 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: COLORY READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/O7/763,352A
FILING DATE: 19910920
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
PEREISTRATION NUMBER: 33,878
PEREISTRATION NUMBER: 33,878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTISAAGVNNWVAQNTE---CTNCAPNFYNN--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FELECOMMUNICATION INFORMATION:
TELEPHONE: 303/499-8080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEX: 823189
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 38.4'
Matches 172; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boulder
STATE: Colorado
COUNTRY: USA
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US-07-763-352A-3
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APPLICANT: CLARK, THOOGORE G.
APPLICANT: CLARK, THOOGORE G.
APPLICANT: CLARK, THOOGORE G.
APPLICANT: Lin, Than-Long
TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF
TITLE OF INVENTION: ICHTHYOPHTHIRIUS
FILE REFERENCE: 235.00170.01
CURRENT APPLICATION NUMBER: US/09/497,967
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1999-04-27
PRIOR FILING DATE: 1999-03-04
PRIOR FILING DATE: 1999-03-04
PRIOR FILING DATE: 1999-03-05
PRIOR FILING DATE: 1999-03-07
SPRIOR FILING DATE: 1999-03-07
SPRIOR FILING DATE: 1999-03-07
SPRIOR FILING DATE: 1999-03-07
SPRIOR FILING DATE: 1999-03-07
SOUTHWARE: PATENTIN VET. 2.1
FYYNGNNGNTPFNPGKSQCTPCPAIKPANVAQATLGNDATITAQCNVACPDGTISAAGVN 252
                                                FYYNGG------SPQGEAPGVQVFAAGAAAGAQANLATQCSNQCPTGTVLDDGVT 167
                                                                                                         253 NWVAQNTE---CTNCAPNFYNN-----NAPN---FNPG------NSTCLPCPANKD 291
                                                                                                                                                                  -- LVFNTSATLCVKCRPNFYYNGGSPQGEAPGVQVFAAGAAAAGVAAVTSQCVPCQLNKN 225
                                                                                                                                                                                                                        YGAEATAGGAATLAKQCNIACPDGTAIASGAT-NYVILQTECLNCAANFYFDGNNFQAGS 350
                                                                                                                                                                                                                                                            SRCKACPANKVQGAVATAGGTATLIAQCALECPAGTVLTDGTTSTYKQAASECVKCAANF 410
                                                                                                                                                                                                                                                                                                                                                                            Sequence 55, Application US/09497967
GENERAL INFORMATION:
APPLICANT: Clark, Theodore G.
APPLICANT: Lin, Tian-Long
TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                165 CPTGTALDDGVTTDYVRSFTECVKCRLNFYYNGNNGNTPFNPGKSQCTPCPAIKPANVAQ 224
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100.0%; Pred. No. 6.7e-29;
Live 0; Mismatches 0;
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RESULT 12
US-09-497-967-60
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Sequence 58, Application US/09497967

GENERAL INFORMATION:

APPLICANT: Clark, Theodore G.

APPLICANT: Dickerson, Jr., Harry W.

APPLICANT: Lin, Tian-Long

TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF

TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF

TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES

FILE REFERENCE: 235.0017010

CURRENT FILING DATE: 2000-02-04

PRIOR PAPLICATION NUMBER: 60/118,634

PRIOR PAPLICATION NUMBER: 60/118,634

PRIOR PELING DATE: 1999-04-27

PRIOR APPLICATION NUMBER: 60/122,372

PRIOR APPLICATION NUMBER: 60/122,372

PRIOR APPLICATION NUMBER: 60/122,372

PRIOR APPLICATION NUMBER: 60/122,372

PRIOR APPLICATION NUMBER: 60/124,905

PRIOR APPLICATION NUMBER: 60/124,905

PRIOR APPLICATION NUMBER: 60/124,905

SOFTWARE: PARENTING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 102

SOFTWARE: PARENTING DATE: 2.1

SEQ ID NO 58

LENGTH: 71
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Best Local Similarity 100.0%; Pred. No. 4.2e-27;
Matches 71; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                15.9%; Score 404; DB 18;
100.0%; Pred. No. 3.5e-27;
Live 0; Mismatches 0;
    FILE REFERENCE: 235.00170101
CURRENT APPLICATION NUMBER: US/09/497,967
CURRENT FILING DATE: 200-02-04
PRIOR APPLICATION NUMBER: 60/134,121
PRIOR FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/118,634
PRIOR APPLICATION NUMBER: 60/122,372
PRIOR FILING DATE: 1999-02-04
PRIOR FILING DATE: 1999-03-02
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PALENTIN VOIN NUMBER: 60/124,905
SEQ ID NO 55
LENGTH: 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT; ORGANISM: Ichthyophthirius multifiliis US-09-497-967-58
                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ; ORGANISM: IChthyophthirius multifiliis US-09-497-967-55
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 15.9
Best Local Similarity 100.
Matches 72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 AATLAKQCNIA 311
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US-09-497-967-58
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                         GENERAL INVORMATION:
APPLICANT: Clark, Theodore G.
APPLICANT: Clark, Tian-Long
APPLICANT: Dickerson, Jr., Harry W.
APPLICANT: Lin, Tian-Long
TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF
TITLE OF INVENTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES:
TITLE OF INVENTION: ICHTHYOPHTHIRIUS
FILE REFERENCE: 235.0017010.
CURRENT PELLICATION NUMBER: 60/131,121
PRIOR FILING DATE: 1999-04-27
PRIOR PAPLICATION NUMBER: 60/131,121
PRIOR APPLICATION NUMBER: 60/118,634
PRIOR PILING DATE: 1999-02-04
PRIOR PILING DATE: 1999-02-04
PRIOR PILING DATE: 1999-03-02
PRIOR PELLING DATE: 1999-03-02
PRIOR FILING DATE: 1999-03-02
PRIOR FILING DATE: 1999-03-02
SOFTWARE: PALENTING NUMBER: 60/124,905
PRIOR FILING DATE: 1999-03-17
SOFTWARE: PALENTING VOT: 2.1
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Best Local Similarity 100.0%; Pred. No. 1.2e-24;
Matches 70; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 389; DB 18;
Pred. No. 7.1e-26;
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100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT CORGANISM: Ichthyophthirius multifiliis US-09-497-967-56
                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Ichthyophthirius multifiliis
; Sequence 60, Application US/09497967; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   442 ESAKKNIQCDFA 453
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Matches 72; Conserva
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US-09-497-967-56
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Search completed: February 11, 2003, 19:53:49 Job time : 143.457 secs
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                                                                                                                                                                         Sequence 59, Application US/09497967
GENERAL INFORMATION:
APPLICANT: Clark, Theedore G.
APPLICANT: Clark, Theedore G.
APPLICANT: Lin, Tian-Long
TITLE OF INVEWTION: DIAGNOSTIC AND PROTECTIVE ANTIGEN GENE SEQUENCES OF
TITLE OF INVENTION: ICHTHYOPHTHIRUS
TITLE OF INVENTION: ICHTHYOPHTHIRUS
FILE REFERENCE: 235.00170101
CURRENT APPLICATION NUMBER: US/09/497,967
CURRENT FILING DATE: 1999-04-27
PRIOR APPLICATION NUMBER: 60/131,121
PRIOR APPLICATION NUMBER: 60/131,23
PRIOR FILING DATE: 1999-02-04
PRIOR FILING DATE: 1999-03-02
PRIOR FILING DATE: 1999-03-03-02
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 102
SOFTWARE: Patentin Ver. 2.1
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95 CPAGTAIAGGATDYAAIITECVNCRINFYNENAPNFNAGASTCTACPVNRVGGALTAGNA 154
                   APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  312 CPDGTAIASGATNYVILQTECLNCAANFYFDGNNFQAGSSRCKACPANKVQGAVATAGGT 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 373; DB 18;
Pred. No. 1.7e-24;
0; Mismatches 0;
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; ORGANISM: Ichthyophthirius multifiliis
US-09-497-967-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 301, Application US/10123155 GENERAL INFORMATION:
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Best Local Similarity 100.0%; P.
Matches 70; Conservative 0;
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Gerritsen, Mary E.
Goddard, Audrey
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Gurney, Austin L.
Sherwood, Steven
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Filvaroff, Ellen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wood, William
                                                                  155 ATIVAÇCNVA 164
                                                                                       61 ATIVAQCNVA 70
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US-10-123-155-301
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US-09-497-967-59
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               282 TCLPCPANKDYGAEATAGGAATLAKQCNIACPDGTAIASGATNYV-ILQTECLNCAANFY 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 ANCVNCQKNFYYNNAAAFVPGASTCTPCPQKKDAGAQPNPPATANLVTQCNVKCPAGTAI 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 AGGATDYAAIITECVNCRINFYNENAPNFNAGASTCTACPVNRVGGALTAGNAATIVAQC 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 NVACPIGTALDDGVTTDYVRSFTECVKCRLNFYYNGNNGNTPFNPGKSQCTPCPAIKPAN 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 -----GAGACAGCCCTGTCTGGACACAG-----AGTTACTGTGGATTTTTAA--GAGAC 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168 TCAGTTAAAG-AATTTAGGAATTTCTGATTCAATTAAAGGATTTACAAATTCATCAACCC 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     341 FDGNNFQAGSSRCKACP--ANKVQGAVATAGGTATLIAQCALECPAGTVLTDGTTSTYKQ 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 AGCATC-----TTAATTTGAATCCAC-----AAAGTTT-----CATGTAA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 TGAAAAGAA-ATACA-----TAATTTTAATTCAAC----CCGAGT-GTTTCCAAG 84
                                                                                                                                                                                                                                                                                                                                    Query Match 10.2%; Score 258; DB 25; Length 1576; Best Local Similarity 29.7%; Pred. No. 1e-12; Matches 118; Conservative 10; Mismatches 175; Indels 94
                                                                                               See Palm or File Wrapper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       399 AASECVKCAANFYTTKQTDWVAGIDTCTSCNKKLTSG 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       279 AAGTC--CAA---TATATGTTATTTTCTTTTTTG 310
                                         US/10/123,155
FILE REFERENCE: P3330R1C30
CURRENT APPLICATION NUMBER: US/10/1
CURRENT FILING DATE: 2002-04-15
Prior Application removed - See Pal
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 301
LENGTH: 1576
                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: HOMO Sapien
US-10-123-155-301
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